

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT:

Seidel, Christoph; Weinhues, Ursula-Henrike;
Schmitt, Urban; Motz, Manfred; Wiedmann, Michael;
Upmeier, Barbara; Soutscheck, Erwin

(ii) TITLE OF INVENTION:

Recombinant antigen from the NS3 region of the hepatitis C virus

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Felfe & Lynch
(B) STREET: 805 Third Avenue
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10022

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: PatentIn Relase #1.0,
Version #1.25 (EPA)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/511,759
(B) FILING DATE: 7-AUGUST-1995

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: p 44 28 705.4
(B) FILING DATE: 12 AUGUST 1994

(ix) ATTORNEY/AGENT INFORMATION

(A) NAME: HANSON, NORMAN
(B) REGISTRATION NUMBER: 30, 946
(C) REFERENCE/DOCKET NUMBER: HUBR 1067.1

(x) TELECOMMUNICATION INFORMATION

(A) TELEPHONE: 212-688-9200
(B) TELEFAX: 212-838-3884

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) INITIAL ORIGIN:

- (A) ORGANISM: hepatitis C virus

(viii) POSITION IN GENOME:

- (A) CHROMOSOME SEGMENT: NS3

(ix) CHARACTERISTICS:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG ACC ATG ATT ACG AAT TCC CGG GGA TCC ATC ATG AAA TCC CCG GTG	48
Met Thr Met Ile Thr Asn Ser Arg Gly Ser Ile Met Lys Ser Pro Val	
1 5 10 15	
ATC ACG GAT AAC TCC TCT CCA CCG GTA GTG CCC CAG AGC TTC CAG GTG	96
Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val	
20 25 30	
GCT CAC CTG CAT GCT CCC ACA GGC AGC GGC AAG AGC ACC AAG GTC CCG	144
Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro	
35 40 45	
GCT GCA TAC GCA GCT CAG GGC TAC AAG GTG CTA GTG CTC AAC CCT TCT	192
Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser	
50 55 60	
GTT GCT GCA ACA TTG GGC TTT GGT GCC TAC ATG TCC AAG GCT CAT GGG	240
Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly	
65 70 75 80	
ATC GAT CCT AAC ATC AGG ACC GGG GTG AGA ACA ATT ACC ACT GGC AGC	288
Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser	
85 90 95	
CCC ATT ACG TAC TCC ACT TAC GGC AAG TTT CTT GCC GAC GGC GGG TGC	336
Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys	
100 105 110	

GCA GGG GGT GCT TAT GAC ATA ATA ATT TGT GAC GAG TGC CAC TCC ACG Ala Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr 115 120 125	384
GAT GCC ACA TCC ATC TTG GGC ATC GGC ACT GTC CTT GAC CAA GGA GAG Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Gly Glu 130 135 140	432
ACT GCG GGG GCG AAA TTG GTT GTG TTC GCC ACC GCC ACC CCT CCG GGC Thr Ala Gly Ala Lys Leu Val Val Phe Ala Thr Ala Thr Pro Pro Gly 145 150 155 160	480
TCC GTC ACT GTG CCC CAT CCC AAC ATT GAG GAG GTT GCT CTA TCC ACC Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr 165 170 175	528
ACC GGA GAG ATC CCT TTT TAC GGC AAG GCT ATC CCC CTT GAG GTA ATC Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile 180 185 190	576
AAG GGG GGG AGA CAT CTC ATC TTC TGT CAT TCA AAG AGG AAG TGC GAT Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Arg Lys Cys Asp 195 200 205	624
GAG CTC GCC ACA AAG CTG GCA ATG GGC ATC AAT GCC GTG GCC TAC Glu Leu Ala Thr Lys Leu Val Ala Met Gly Ile Asn Ala Val Ala Tyr 210 215 220	672
TAC CGC GGT CTT GAC GTG TCC GTC ATC CCG ACC AGC GGT GAT GTT GTC Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val 225 230 235 240	720
GTC GTG GCA ACC GAC GCC CTC ATG ACC GGC TAT ACC GGC GAC TTC GAC Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp 245 250 255	768
TCG GTG ATA GAC TGC AAC ACG TGT GTC ACT CAG ACA GTC GAT TTC AGC Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser 260 265 270	816
CTT GAC CCT ACC TTC ACC ATT GAG ACG ACC ACA CTT CCC CAG GAT GCT Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Leu Pro Gln Asp Ala 275 280 285	864
GTC TCC CGC ACT CAA CGA CGG Val Ser Arg Thr Gln Arg Arg 290 295	885

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Met Ile Thr Asn Ser Arg Gly Ser Ile Met Lys Ser Pro Val
1 5 10 15

Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val
20 25 30

Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro
35 40 45

Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser
50 55 60

Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly
65 70 75 80

Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser
85 90 95

Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys
100 105 110

Ala Gly Gly Ala Tyr Asp Ile Ile Cys Asp Glu Cys His Ser Thr
115 120 125

Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Gly Glu
130 135 140

Thr Ala Gly Ala Lys Leu Val Val Phe Ala Thr Ala Thr Pro Pro Gly
145 150 155 160

Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr
165 170 175

Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile
180 185 190

Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Arg Lys Cys Asp
195 200 205

Glu Leu Ala Thr Lys Leu Val Ala Met Gly Ile Asn Ala Val Ala Tyr
210 215 220
Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val
225 230 235 240
Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp
245 250 255
Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser
260 265 270
Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Leu Pro Gln Asp Ala
275 280 285
Val Ser Arg Thr Gln Arg Arg
290 295

(4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAGGGATCCA TCATGAAATC CCCGGTGTTC ACGGATAACT

40

(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGGAAGCCTT AATTCTTACC GTCGTTGAGT GCAGGAGAC

(6) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GAGGGATCCA TCATGAAAGC GGTGGACTTT ATCCCTGTG

39

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GAGAAGCTTT TAACACGTGT TGCAGTCTAT CAC

33

(8) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GAGGGATCCA TCATGAAACA CCTGCATGCT CCCACCGGC

39

(8) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GAGAAGCTTT TAATACCAAG CACAGCCTGC GTC

33

(3) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Pro Val Glu Asn Leu Glu Thr Thr Met Arg Ser Pro Val Phe Thr
1 5 10 15

13. assm 2 Thr¹⁴ forward in 2

Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val Ala
20 25 30

His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro
35 40 45

Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro
50 55 60

Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala
65 70 75

His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr
80 85 90

Thr Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala
95 100 105

Asp Gly Gly Cys Ala Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp
110 115 120

Glu Cys His Ser Thr Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr
125 130 135

Val Leu Asp Gln Gly Glu Thr Ala Gly Ala Lys Leu Val Val Phe
140 145 150

Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn
155 160 165

Ile Glu Glu Val Ala Leu Ser Thr Thr Gly Glu Ile Pro Phe Tyr
170 175 180

Gly Lys Ala Ile Pro Leu Glu Val Ile Lys Gly Gly Arg His Leu
185 190 195

Ile Phe Cys His Ser Lys Arg Lys Cys Asp Glu Leu Ala Thr Lys
200 205 210

Leu Val Ala Met Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu
215 220 225

Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val Val Val Ala
230 235 240

Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val
245 250 255

Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu
260 265 . 270

Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Leu Pro Gln Asp Ala
275 280 285

Val Ser Arg Thr Gln Arg Arg Gly Arg Thr Gly Arg Gly Lys Pro
290 | 295 300

Gly Ile
302

SEQUENCE PROTOCOL

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Boehringer Mannheim GmbH
- (B) ROAD: Sandhofer Str. 112-132
- (C) CITY: Mannheim
- (E) COUNTRY: Germany
- (F) POSTAL CODE: 68305

(ii) TITLE OF APPLICATION: Recombinant antigen from
the NS3 region of the hepatitis C virus

(iii) NUMBER OF SEQUENCES: 8

(iv) COMPUTER READABLE FORM:

- (A) DATA CARRIER: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0,
Version #1.25 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRAND FORM: both
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: cDNA

(vi) INITIAL ORIGIN:

(A) ORGANISM: hepatitis C virus

(viii) POSITION IN THE GENOME:

(A) CHROMOSOME/SEGMENT: NS3

(ix) CHARACTERISTICS:

(A) NAME/KEY: CDS

(B) LOCATION: 1..885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATG ACC ATG ATT ACG AAT TCC CCG GGA TCC ATC ATG AAA TCC CCG GTG	48
Met Thr Met Ile Thr Asn Ser Arg Gly Ser Ile Met Lys Ser Pro Val	
1 5 10 15	
TTC ACG GAT AAC TCC TCT CCA CCG GTA GTG CCC CAG AGC TTC CAG GTG	96
Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val	
20 25 30	
GCT CAC CTG CAT GCT CCC ACA GGC AGC GGC AAG AGC ACC AAG GTC CCG	144
Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro	
35 40 45	
GCT GCA TAC GCA GCT CAG GGC TAC AAG GTG CTA GTG CTC AAC CCT TCT	192
Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser	
50 55 60	
GTT GCT GCA ACA TTG GGC TTT GGT GCC TAC ATG TCC AAG GCT CAT GGG	240
Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly	
65 70 75 80	
ATC GAT CCT AAC ATC AGG ACC GGG GTG AGA ACA ATT ACC ACT GGC AGC	288
Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser	
85 90 95	
CCC ATT ACG TAC TCC ACT TAC GGC AAG TTT CTT GCC GAC GGC GGG TGC	336
Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys	
100 105 110	
GCA GGG GGT GCT TAT GAC ATA ATA ATT TGT GAC GAG TGC CAC TCC ACG	384
Ala Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr	
115 120 125	
GAT GCC ACA TCC ATC TTG GGC ATC GGC ACT GTC CTT GAC CAA GGA GAG	432
Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Gly Glu	
130 135 140	

ACT GCG GGG GCG AAA TTG GTT GTG TTC GCC ACC GCC ACC CTC CCG GGC Thr Ala Gly Ala Lys Leu Val Val Phe Ala Thr Ala Thr Pro Pro Gly 145 150 155 160	480
TCC GTC ACT GTG CCC CAT CCC AAC ATT GAG GAG GTT GCT CTA TCC ACC Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr 165 170 175	528
ACC GGA GAG ATC CCT TTT TAC GGC AAG GCT ATC CCC CTT GAG GTA ATC Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile 180 185 190	576
AAG GGG GGG AGA CAT CTC ATC TTC TGT CAT TCA AAG AGG AAG TGC GAT Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Arg Lys Cys Asp 195 200 205	624
GAG CTC GCC ACA AAG CTG GTC GCA ATG GGC ATC AAT GCC GTG GCC TAC Glu Leu Ala Thr Lys Leu Val Ala Met Gly Ile Asn Ala Val Ala Tyr 210 215 220	672
TAC CGC GGT CTT GAC GTG TCC GTC ATC CCG ACC AGC GGT GAT GTT GTC Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val 225 230 235 240	720
GTC GTG GCA ACC GAC GCC CTC ATG ACC GGC TAT ACC GGC GAC TTC GAC Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp 245 250 255	768
TCG GTG ATA GAC TGC AAC ACG TGT GTC ACT CAG ACA GTC GAT TTC AGC Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser 260 265 270	816
CTT GAC CCT ACC TTC ACC ATT GAG ACG ACC ACA CTT CCC CAG GAT GCT Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Leu Pro Gln Asp Ala 275 280 285	864
GTC TCC CGC ACT CAA CGA CGG Val Ser Arg Thr Gln Arg Arg 290 295	885

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Met Ile Thr Asn Ser Arg Gly Ser Ile Met Lys Ser Pro Val

1

5

10

15

Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val
20 25 30

Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro
35 40 45

Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser
50 55 60

Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly
65 70 75 80

Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser
85 90 95

Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys
100 105 110

Ala Gly Gly Ala Tyr Asp Ile Ile Cys Asp Glu Cys His Ser Thr
115 120 125

Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Gly Glu
130 135 140

Thr Ala Gly Ala Lys Leu Val Val Phe Ala Thr Ala Thr Pro Pro Gly
145 150 155 160

Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr
165 170 175

Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile
180 185 190

Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Arg Lys Cys Asp
195 200 205

Glu Leu Ala Thr Lys Leu Val Ala Met Gly Ile Asn Ala Val Ala Tyr
210 215 220

Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val
225 230 235 240

Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp
245 250 255

Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser
260 265 270

Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Leu Pro Gln Asp Ala
275 280 285

Val Ser Arg Thr Gln Arg Arg
290 295

1

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRAND FORM: single
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAGGGATCCA TCATGAAATC CCCGGTGTTC ACGGATAACT

40

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRAND FORM: single
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

GGGAAGCCTT AATTCTTACC GTCGTTGAGT GCGGGAGAC

39

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRAND FORM: single

09856022-000001
(D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

GAGGGATCCA TCATGAAAGC GGTGGACTTT ATCCCTGTG

39

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRAND FORM: single
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

GAGAAGCTTT TAACACGTGT TGCAGTCTAT CAC

33

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRAND FORM: single
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GAGGGATCCA TCATGAAACA CCTGCATGCT CCCACCGGC

39

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRAND FORM: single
- (D) TOPOLOGY: linear

(ii) TYPE OF MOLECULE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

GAGAAGCTTT TAATACCAAG CACAGCCTGC GTC

33